



# results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,  
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),  
"Gapped BLAST and PSI-BLAST: a new generation of protein database search  
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1109960786-8874-77563893168.BLASTQ2

Query=

(60 letters)

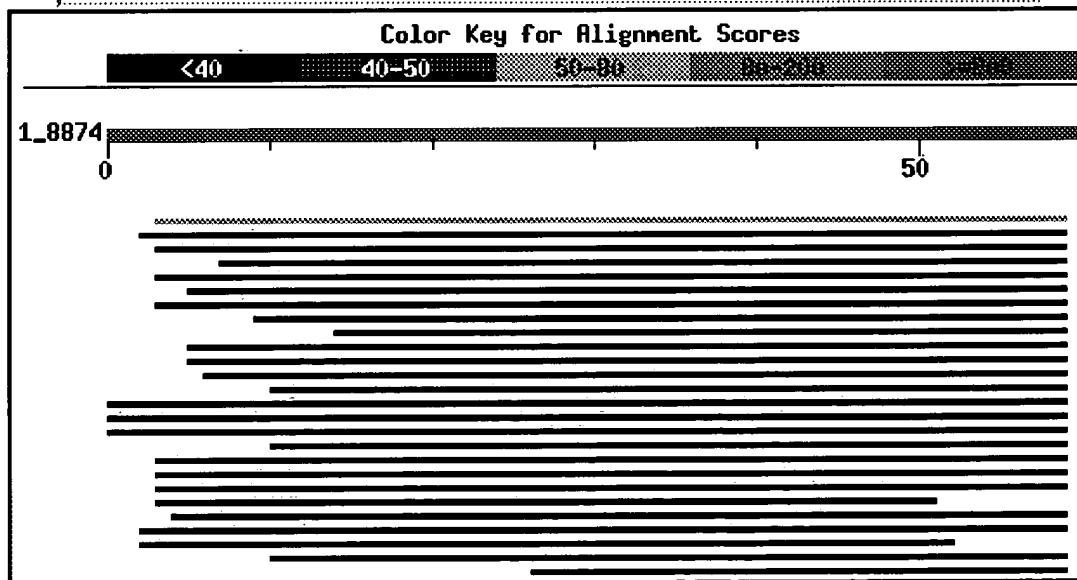
**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
2,340,000 sequences; 793,074,205 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 26 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score (bits)  
E Value

gi 46580775 ref YP_011583.1	outer membrane protein OmpH, p...	55	7e-07	G
gi 54030341 ref ZP_00362479.1	COG2825: Outer membrane prot...	39	0.030	
gi 28851988 gb AAO55063.1	outer membrane protein OmpH, put...	39	0.039	G
gi 48732730 ref ZP_00266473.1	COG2825: Outer membrane prot...	39	0.052	
gi 48768198 ref ZP_00272549.1	COG2825: Outer membrane prot...	38	0.088	
gi 47575422 ref ZP_00245457.1	COG2825: Outer membrane prot...	38	0.088	
gi 26988332 ref NP_743757.1	outer membrane protein OmpH [P...	37	0.15	G

<u>gi 46188414 ref ZP_00125848.2 </u>	COG2825: Outer membrane prot...	<u>37</u>	0.20	
<u>gi 41725330 ref ZP_00152088.1 </u>	COG2825: Outer membrane prot...	<u>36</u>	0.33	
<u>gi 33596183 ref NP_883826.1 </u>	putative outer membrane protei...	<u>35</u>	0.57	<span style="background-color: #008000; color: black;">G</span>
<u>gi 33592526 ref NP_880170.1 </u>	putative outer membrane protei...	<u>35</u>	0.57	<span style="background-color: #008000; color: black;">G</span>
<u>gi 17428428 emb CAD15115.1 </u>	PROBABLE TRANSMEMBRANE PROTEIN ...	<u>35</u>	0.57	<span style="background-color: #008000; color: black;">G</span>
<u>gi 48787685 ref ZP_00283664.1 </u>	COG2825: Outer membrane prot...	<u>34</u>	1.3	
<u>gi 52006428 ref ZP_00333808.1 </u>	COG2825: Outer membrane prot...	<u>33</u>	1.7	
<u>gi 53719759 ref YP_108745.1 </u>	putative outer membrane protei...	<u>33</u>	2.8	<span style="background-color: #008000; color: black;">G</span>
<u>gi 9949807 gb AAG07035.1 </u>	probable outer membrane protein p...	<u>33</u>	2.8	<span style="background-color: #008000; color: black;">G</span>
<u>gi 49081394 gb AAT50125.1 </u>	PA3647 [synthetic construct]	<u>33</u>	2.8	
<u>gi 51597309 ref YP_071500.1 </u>	cationic 19 kDa outer membrane...	<u>32</u>	4.8	<span style="background-color: #008000; color: black;">G</span>
<u>gi 45442565 ref NP_994104.1 </u>	cationic 19 kDa outer membrane...	<u>32</u>	4.8	<span style="background-color: #008000; color: black;">G</span>
<u>gi 16121353 ref NP_404666.1 </u>	cationic 19 kDa outer membrane...	<u>32</u>	4.8	<span style="background-color: #008000; color: black;">G</span>
<u>gi 51246715 ref YP_066599.1 </u>	hypothetical protein DP2863 [D...	<u>32</u>	4.8	<span style="background-color: #008000; color: black;">G</span>
<u>gi 46164357 ref ZP_00205054.1 </u>	COG2825: Outer membrane prot...	<u>32</u>	4.8	
<u>gi 30249671 ref NP_841741.1 </u>	putative transmembrane protein...	<u>32</u>	6.3	<span style="background-color: #008000; color: black;">G</span>
<u>gi 34103516 gb AAQ59878.1 </u>	outer membrane protein [Chromoba...	<u>32</u>	6.3	<span style="background-color: #008000; color: black;">G</span>
<u>gi 46319050 ref ZP_00219470.1 </u>	COG2825: Outer membrane prot...	<u>32</u>	6.3	
<u>gi 53761352 ref ZP_00166830.2 </u>	COG2825: Outer membrane prot...	<u>31</u>	8.2	

### Alignments

[Get selected sequences](#)     [Select all](#)     [Deselect all](#)

>gi|46580775|ref|YP\_011583.1| G outer membrane protein OmpH, putative [Desulfovibrio vulgaris str. Hildenborough]  
gi|46450195|gb|AAS96843.1| G outer membrane protein OmpH, putative [Desulfovibrio vulgaris str. Hildenborough]  
Length = 175

Score = 54.7 bits (130), Expect = 7e-07  
Identities = 26/57 (45%), Positives = 39/57 (68%)

Query: 4 KTLSMAILACLLVANSAFSADFPPIGVFNSQSIAAMESEAAKAAQKKLQSEFGNEKTQL 60  
K L A+ A L+ A++A +AD +G+ N Q +A + EAA+ AQKK+++ FG EK QL  
Sbjct: 3 KILVFAVAALMAASTAMAADLKVGIVNMQKLATQCEAAQEAQKKMKATFGPEKDQL 59

>gi|54030341|ref|ZP\_00362479.1| COG2825: Outer membrane protein [Polaromonas sp.]  
Length = 168

Score = 39.3 bits (90), Expect = 0.030  
Identities = 23/61 (37%), Positives = 34/61 (55%), Gaps = 3/61 (4%)

Query: 3 VKTLSMAILACLLVANSAFSA---DFPIGVFNSQSIAAMESEAAKAAQKKLQSEFGNEKTQ 59  
+K S I ++A + FSA +F +GV N I E+ +AKAAQ KL+ EF ++  
Sbjct: 1 MKHFSTKIFLGCVIALAGFSASAQEFKVGVVNLDRIFREANSAKAAQTKLEQFSKREKE 60

Query: 60 L 60  
L  
Sbjct: 61 L 61

>gi|28851988|gb|AA055063.1| G outer membrane protein OmpH, putative [Pseudomonas tomato str. DC3000]  
gi|28868749|ref|NP\_791368.1| G outer membrane protein OmpH, putative [Pseudomonas tomato str. DC3000]

Length = 167

Score = 38.9 bits (89), Expect = 0.039  
Identities = 23/57 (40%), Positives = 33/57 (57%), Gaps = 1/57 (1%)

Query: 4 KTLSMAILACLLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
K + +LA +LVA+ AF AD I V N Q +ES+AAK + +FG + T+L  
Sbjct: 3 KLTQLVLLATVLVASPAF-ADMKIAVLNYQMALLESDAAKKYAVDAEKKFGPQLTKL 58

[>gi|48732730|ref|ZP\_00266473.1| COG2825: Outer membrane protein [Pseudomonas fl]

Length = 161

Score = 38.5 bits (88), Expect = 0.052  
Identities = 23/53 (43%), Positives = 31/53 (58%), Gaps = 1/53 (1%)

Query: 8 MAILACLLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
M +LA +LVA AF AD I V N Q +ES+AAK + +FG + T+L  
Sbjct: 1 MVLLASVLVAGPAF-ADMKIAVLNYQMALLESDAAKKYAVDAEKKFGPQLTKL 52

[>gi|48768198|ref|ZP\_00272549.1| COG2825: Outer membrane protein [Ralstonia meta]

Length = 177

Score = 37.7 bits (86), Expect = 0.088  
Identities = 24/59 (40%), Positives = 32/59 (54%), Gaps = 2/59 (3%)

Query: 4 KTLSMAILAC--LLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
K+LS A LA L A A + + I NS+ I +S+ AKAAQ KL+ EF +L  
Sbjct: 9 KSLSAAAALAAAALCAAAAPAMAQEARIAAVN SERILRDSQPAKAAQVKLEQEF SKRDREL 67

[>gi|47575422|ref|ZP\_00245457.1| COG2825: Outer membrane protein [Rubrivivax gel

Length = 163

Score = 37.7 bits (86), Expect = 0.088  
Identities = 22/55 (40%), Positives = 33/55 (60%), Gaps = 2/55 (3%)

Query: 6 LSMAILACLLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
L+ A+LA + A +A + IG NS+ + E+ AKAAQ KL+SEF + +L  
Sbjct: 4 LAAAVLAAGVTAAAA--QELKIGYVN SERVLREAGPAKAAQAKLESEFSKREKEL 56

[>gi|26988332|ref|NP\_743757.1| G outer membrane protein OmpH [Pseudomonas putida

gi|24983081|gb|AAN67221.1| G outer membrane protein OmpH [Pseudomonas putida KT24

Length = 167

Score = 37.0 bits (84), Expect = 0.15  
Identities = 21/57 (36%), Positives = 32/57 (56%), Gaps = 1/57 (1%)

Query: 4 KTLSMAILACLLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
K +A++A LVA AF A+ + V N Q +ES+AAK + +FG + T+L  
Sbjct: 3 KLAQLAVVAAALVATPAF-AEMKAVLNYQMALLESDAAKKYAVDAEKKFGPQLTKL 58

[>gi|46188414|ref|ZP\_00125848.2| COG2825: Outer membrane protein [Pseudomonas sy

syringae B728a]

Length = 159

Score = 36.6 bits (83), Expect = 0.20

Identities = 22/51 (43%), Positives = 31/51 (60%), Gaps = 1/51 (1%)

Query: 10 ILACLLVANSASFADFPPIGVFNSOSIAMESEAAKAAQKKLOSEFGNEKTQL 60

+LA +LVA+ AF AD I V N Q +ES+AAK + +FG + T+L

Sbjct: 1 MLATVLVSPAF-ADMKIAVLNYQMALLESDAAKRYAVDAEKKFGPQLTKL 50

[>gi|41725330|ref|ZP\_00152088.1| COG2825: Outer membrane protein [Dechloromonas :  
Length = 156

Score = 35.8 bits (81), Expect = 0.33

Identities = 17/46 (36%), Positives = 26/46 (56%)

Query: 15 LVANSASFADFPPIGVFNSOSIAMESEAAKAAQKKLQSEFGNEKTQL 60

L A A++A+ +G N+Q I ++ AA+ A KKL+ EF L

Sbjct: 4 LFATGAYAAELKVGYVNTQRIFRDAPAAQKAACKLEGEFAKRDQDL 49

[>gi|33596183|ref|NP\_883826.1| G putative outer membrane protein [Bordetella par  
gi|33573186|emb|CAE36838.1| G putative outer membrane protein [Bordetella paraper  
Length = 203

Score = 35.0 bits (79), Expect = 0.57

Identities = 22/59 (37%), Positives = 32/59 (54%), Gaps = 4/59 (6%)

Query: 6 LSMAILACLLVANSAF----SADFPPIGVFNSOSIAMESEAAKAAQKKLQSEFGNEKTQL 60

+S+A+ LL +SA + IG N++ I ES AKAAQ K++SEF +L

Sbjct: 40 VSIALAGALLFGSSAAVTAQAQGKIGFVNTERILRESPAKAAQSKIESEFKRRDDEL 98

[>gi|33592526|ref|NP\_880170.1| G putative outer membrane protein [Bordetella pert  
gi|33601591|ref|NP\_889151.1| G putative outer membrane protein [Bordetella bronch  
gi|33576027|emb|CAE33107.1| G putative outer membrane protein [Bordetella bronchi  
gi|33572172|emb|CAE41718.1| G putative outer membrane protein [Bordetella pertuss  
Length = 187

Score = 35.0 bits (79), Expect = 0.57

Identities = 22/59 (37%), Positives = 32/59 (54%), Gaps = 4/59 (6%)

Query: 6 LSMAILACLLVANSAF----SADFPPIGVFNSOSIAMESEAAKAAQKKLQSEFGNEKTQL 60

+S+A+ LL +SA + IG N++ I ES AKAAQ K++SEF +L

Sbjct: 24 VSIALAGALLFGSSAAVTAQAQGKIGFVNTERILRESPAKAAQSKIESEFKRRDDEL 82

[>gi|17428428|emb|CAD15115.1| G PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanac  
gi|17546132|ref|NP\_519534.1| G PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanace  
Length = 184

Score = 35.0 bits (79), Expect = 0.57

Identities = 20/54 (37%), Positives = 29/54 (53%)

Query: 7 SMAILACLLVANSASFADFPPIGVFNSOSIAMESEAAKAAQKKLQSEFGNEKTQL 60

+ A LA A A + + I NS+ I +S+ AKAAQ KL++EF +L

Sbjct: 21 AFAALAAAASFALPATAQEARIAAVNSERILRDSQPAKAAQAKLETEFAKRDREL 74

[>gi|48787685|ref|ZP\_00283664.1| COG2825: Outer membrane protein [Burkholderia f  
Length = 169

Score = 33.9 bits (76), Expect = 1.3  
Identities = 21/50 (42%), Positives = 24/50 (48%)

Query: 11 LACLLVANSAFSADFPPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
LA L A + I NS I ES AAKAAQ KL++EF L  
Sbjct: 12 LAMTLGVGVAHGQEARIAAVNSDRILRESAAKAAQVKLEAEFAKRDKDL 61

[>gi|52006428|ref|ZP\_00333808.1| COG2825: Outer membrane protein [Thiobacillus de  
25259]  
Length = 167

Score = 33.5 bits (75), Expect = 1.7  
Identities = 17/60 (28%), Positives = 29/60 (48%)

Query: 1 MKVKTLSMAILACLLVANSAFSADFPPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
M K +++++ AD IG N++ + E+ + AAQKKL+ EF +L  
Sbjct: 2 MSFKQFALSIMLATAFVAMPAGADTKIGFVNTERLLREAPLSVAAQKKLEREFAGRQEL 61

[>gi|53719759|ref|YP\_108745.1| G putative outer membrane protein [Burkholderia ps  
K96243]

gi|53723730|ref|YP\_103186.1| G outer membrane protein, OmpH/HlpA family [Burkholde  
ATCC 23344]

gi|52427153|qb|AAU47746.1| G outer membrane protein, OmpH/HlpA family [Burkholder  
ATCC 23344]

gi|52210173|emb|CAH36152.1| G putative outer membrane protein [Burkholderia pseud  
K96243]  
Length = 177

Score = 32.7 bits (73), Expect = 2.8  
Identities = 22/51 (43%), Positives = 26/51 (50%), Gaps = 1/51 (1%)

Query: 11 LACLLVANSAFSADFP-IGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
LA L A +A + D I NS I ES AAKAAQ KL++EF L  
Sbjct: 16 LAAALGATAARAQDVARIAAVNSDRILRESAPAKAAQTKLEAEFAKRDKDL 66

[>gi|9949807|qb|AAG07035.1| G probable outer membrane protein precursor [Pseudomonas  
PAO1]

gi|11351575|pir||G83190 probable outer membrane protein precursor PA3647 [imported  
Pseudomonas aeruginosa (strain PAO1)]

gi|20139187|sp|Q9HXY5|OMPH\_PSEAE OmpH-like protein precursor

gi|15598843|ref|NP\_252337.1| G probable outer membrane protein precursor [Pseudomonas  
PAO1]  
Length = 168

Score = 32.7 bits (73), Expect = 2.8  
Identities = 21/60 (35%), Positives = 32/60 (53%), Gaps = 1/60 (1%)

Query: 1 MKVKTLSMAILACLLVANSAFSADFPPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
M+ T + I A ++ A SAF A+ I V N Q +ES+AAK + +FG + +L  
Sbjct: 1 MRKFTQFVLITAAIMAAPS AF-AEMKIAVLNYQM ALLESDAAKQYAVDAEKKFGPQLNKL 59

[>gi|49081394|qb|AAT50125.1| PA3647 [synthetic construct]  
Length = 169

Score = 32.7 bits (73), Expect = 2.8  
Identities = 21/60 (35%), Positives = 32/60 (53%), Gaps = 1/60 (1%)

Query: 1 MKVKTLSMAILACLLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
M+ T + I A ++ A SAF A+ I V N Q +ES+AAK + +FG + +L  
Sbjct: 1 MRKFTQFVLITAAIMAAPSAF-AEMKIAVLNYQMALLESDAAKQYAVDAEKKFGPQLNKL 59

[>gi|51597309|ref|YP\_071500.1| G cationic 19 kDa outer membrane protein precursor; pseudotuberculosis IP 32953]  
gi|51590591|emb|CAH22232.1| G cationic 19 kDa outer membrane protein precursor [Y pseudotuberculosis IP 32953]  
Length = 182

Score = 32.0 bits (71), Expect = 4.8  
Identities = 19/57 (33%), Positives = 29/57 (50%)

Query: 4 KTLMSMAILACLLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
K L A L L A+++ A I + N SI + A +A K+L++EF T+L  
Sbjct: 20 KWLCASLGLALAASASVQAADKIAIVNVSSIFQQLPAREAVAKQLENEFKGRATEL 76

[>gi|45442565|ref|NP\_994104.1| G cationic 19 kDa outer membrane protein precursor; biovar Medievalis str. 91001]  
gi|22127002|ref|NP\_670425.1| G automembrane protein H [Yersinia pestis KIM]  
gi|45437430|gb|AAS62981.1| G cationic 19 kDa outer membrane protein precursor [Ye biovar Medievalis str. 91001]  
gi|21960048|gb|AAM86676.1| G automembrane protein H [Yersinia pestis KIM]  
Length = 196

Score = 32.0 bits (71), Expect = 4.8  
Identities = 19/57 (33%), Positives = 29/57 (50%)

Query: 4 KTLMSMAILACLLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
K L A L L A+++ A I + N SI + A +A K+L++EF T+L  
Sbjct: 34 KWLCASLGLALAASASVQAADKIAIVNVSSIFQQLPAREAVAKQLENEFKGRATEL 90

[>gi|16121353|ref|NP\_404666.1| G cationic 19 kDa outer membrane protein precursor; CO92]  
gi|15979120|emb|CAC89895.1| G cationic 19 kDa outer membrane protein precursor [Y CO92]  
gi|20138917|sp|P58607|OMPH\_YERPE Cationic 19 kDa outer membrane protein precursor  
gi|55977788|sp|P31520|OMPH\_YERPS Cationic 19 kDa outer membrane protein precursor  
gi|25294338|pir||AD0129 cationic 19 kDa outer membrane protein precursor ompH [im - Yersinia pestis (strain CO92)]  
Length = 165

Score = 32.0 bits (71), Expect = 4.8  
Identities = 19/57 (33%), Positives = 29/57 (50%)

Query: 4 KTLMSMAILACLLVANSAFSADFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
K L A L L A+++ A I + N SI + A +A K+L++EF T+L  
Sbjct: 3 KWLCASLGLALAASASVQAADKIAIVNVSSIFQQLPAREAVAKQLENEFKGRATEL 59

[>gi|51246715|ref|YP\_066599.1| G hypothetical protein DP2863 [Desulfotalea psychi]  
gi|50877752|emb|CAG37592.1| G unknown protein [Desulfotalea psychrophila LSv54]  
Length = 185

Score = 32.0 bits (71), Expect = 4.8  
Identities = 17/50 (34%), Positives = 31/50 (62%), Gaps = 1/50 (2%)

Query: 4 KTLSMAILA-CLLVANSAFSADFPPIGVFNSQSIAMESEAAKAAQKKLQSE 52  
K+L + +L+ C L +SA++A IGV + Q I E +A K A +++++  
Sbjct: 16 KSLFVVVLSVCALFVSSAYAAVTKIGVMDVQKIIITECKAGKTASARVEAK 65

[>gi|46164357|ref|ZP\_00205054.1] COG2825: Outer membrane protein [Pseudomonas aeruginosa UCBPP-PA14]  
Length = 173

Score = 32.0 bits (71), Expect = 4.8  
Identities = 20/56 (35%), Positives = 30/56 (53%), Gaps = 1/56 (1%)

Query: 5 TLSMAILACLLVANSAFSADFPPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
T + I A ++ A SAF A+ I V N Q +ES+AAK + +FG + +L  
Sbjct: 10 TQFVLITAAIMAAPSAF-AEMKIAVLNYQMALLESDAAKQYAVDAEKKFGPQLNKL 64

[>gi|30249671|ref|NP\_841741.1] G putative transmembrane protein [Nitrosomonas europa]  
[>gi|30180708|emb|CAD85620.1] G putative transmembrane protein [Nitrosomonas europaea]  
Length = 187

Score = 31.6 bits (70), Expect = 6.3  
Identities = 19/51 (37%), Positives = 29/51 (56%), Gaps = 2/51 (3%)

Query: 3 VKTLSMAILACLLVANSAFSADFPPIGVFNSQSIAMESEAAKAAQKKLQSEF 53  
VK + ++ L V +SA + IGV N++ + ES A AQKK++ EF  
Sbjct: 17 VKAFVVTMMFVLPVHSSA--GEIKIGVVNTEKVLRESMPAIEAQKKIEREF 65

[>gi|34103516|gb|AAQ59878.1] G outer membrane protein [Chromobacterium violaceum]  
[>gi|34497660|ref|NP\_901875.1] G outer membrane protein [Chromobacterium violaceum]  
Length = 161

Score = 31.6 bits (70), Expect = 6.3  
Identities = 17/58 (29%), Positives = 28/58 (48%)

Query: 3 VKTLSMAILACLLVANSAFSADFPPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
+K L + + A +ADF +G N + I E+ + A KKL EF + + +L  
Sbjct: 1 MKALKWWLAVLSVAALPVHAADFKLGFVNIERIYREAGVSVAIYKKLDKEFSSRREEL 58

[>gi|46319050|ref|ZP\_00219470.1] COG2825: Outer membrane protein [Burkholderia cepacia]  
Length = 166

Score = 31.6 bits (70), Expect = 6.3  
Identities = 21/51 (41%), Positives = 26/51 (50%), Gaps = 1/51 (1%)

Query: 11 LACLLVANSAFSADFP-IGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
+A L A +A + D I NS I ES AKAAQ KL++EF L  
Sbjct: 7 IALALGAATAHAQDVARIAAVNSDRILRESAPAKAAQTKLEAEFAKRDKDL 57

[>gi|53761352|ref|ZP\_00166830.2] COG2825: Outer membrane protein [Ralstonia eutropha]  
Length = 148

Score = 31.2 bits (69), Expect = 8.2  
Identities = 15/34 (44%), Positives = 20/34 (58%)

Query: 27 IGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60  
I NS+ I +S+ AKAAQ KL+ EF +L

**Get selected sequences****Select all****Deselect all**

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Mar 3, 2005 10:03 AM

Number of letters in database: 793,074,205

Number of sequences in database: 2,340,000

Lambda	K	H
0.315	0.123	0.314

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 14,682,859

Number of Sequences: 2340000

Number of extensions: 305533

Number of successful extensions: 1709

Number of sequences better than 10.0: 7

Number of HSP's better than 10.0 without gapping: 4

Number of HSP's successfully gapped in prelim test: 3

Number of HSP's that attempted gapping in prelim test: 1705

Number of HSP's gapped (non-prelim): 7

length of query: 60

length of database: 793,074,205

effective HSP length: 32

effective length of query: 28

effective length of database: 718,194,205

effective search space: 20109437740

effective search space used: 20109437740

T: 11

A: 40

X1: 16 ( 7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.6 bits)

S2: 69 (31.2 bits)